

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 23:34:06 ; Search time 329.348 Seconds
(without alignments)
368.000 Million cell updates/sec

Title: US-09-355-254f-22
Perfect score: 20
Sequence: 1 aagcgaaatgaaattgact 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications NA:**
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq**
2: /cgn2_6/ptodata/2/pubpna/FCT_NEW_PUB.seq**
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq**
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq**
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq**
6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq**
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq**
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq**
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq**
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq**
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq**
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq**
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq**
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq**
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq**
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq**
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq**
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq**
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq**
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq**
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq**
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 21:29:42 ; Search time 424.565 Seconds
(without alignments)
71.224 Million cell updates/sec

Title: US-09-355-254F-22
Perfect score: 20
Sequence: 1 aagcgaaatgaattgact 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9120346 seqs, 755981628 residues

Total number of hits satisfying chosen parameters: 18240692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq2:*
3: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq2:*
9: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq3:*
10: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq4:*
11: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq5:*
12: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

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and is derived by analysis of the total score distribution.

STIMMADVT

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OM-nucleic - nucleic search, using sw model

Run on: April 10, 2005, 19:59:00 ; Search time 48.6956 Seconds
(without alignments)
672.042 Million cell updates/sec

Title: US-09-355-254F-22
Perfect score: 20
Sequence: 1 aagcgaaatgaattgact 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
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Mon Apr 11 17:01:09 2005

us-09-355-254f-22.rnppm

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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 20:43:46 ; Search time 2170.87 Seconds
(without alignments)
376.099 Million cell updates/sec

Title: US-09-355-254F-22
Perfect score: 20
Sequence: 1 aagcgaaatgaaattgact 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Pending_Patents_NA Main:*

Mon Apr 11 17:01:10 2005

us-09-355-254f-22.rst

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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 18:43:41 ; Search time 1477.46 Seconds
(without alignments)
515.265 Million cell updates/sec

Title: US-09-355-254F-22
Perfect score: 20
Sequence: 1 aagcgaaatgaaattgact 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ga81:*
9: gb_ga82:*

Pred. No. is the number of results predicted by chance to have a
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STANDARD

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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 11:44:31 ; Search time 162.246 Seconds
(without alignments)
729.722 Million cell updates/sec

Title: US-09-355-254F-22
Perfect score: 20
Sequence: 1 aagcgaaatgaaattgact 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 439206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

- Database : N_Geneseq_16Dec04:*
- 1: Geneseqn1980s:*
 - 2: Geneseqn1990s:*
 - 3: Geneseqn2000s:*
 - 4: Geneseqn2001as:*
 - 5: Geneseqn2001bs:*
 - 6: Geneseqn2002as:*
 - 7: Geneseqn2002bs:*
 - 8: Geneseqn2003as:*
 - 9: Geneseqn2003bs:*
 - 10: Geneseqn2003cs:*
 - 11: Geneseqn2003ds:*
 - 12: Geneseqn2004as:*
 - 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 11:53:15 ; Search time 511.449 Seconds
(without alignments)
1894.820 Million cell updates/sec

Title: US-09-355-254F-22

Perfect score: 20

Sequence: 1 aagcgaaatgaaattgact 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result